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US-09-988-201-5
Title:
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                                                                  BCT 21-APR-1994
            ACCGKAB
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                                                 DNA
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LOCUS
            A.carrageenovora genes cgkA and cgkB, partial.
DEFINITION
ACCESSION
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VERSION
KEYWORDS
            kappa-carrageenase.
SOURCE
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  ORGANISM
            Pseudoalteromonas carrageenovora
            Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
            Alteromonadaceae; Pseudoalteromonas.
REFERENCE
            Barbeyron, T., Henrissat, B. and Kloareg, B.
  AUTHORS
            The gene encoding the kappa-carrageenase of Alteromonas
  TITLE
            carrageenovora is related to beta-1, 3-1, 4-glucanases
            Gene 139 (1), 105-109 (1994)
  JOURNAL
  MEDLINE
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   PUBMED
            8112578
REFERENCE
               (bases 1 to 2180)
  AUTHORS
            Barbeyron, T.
  TITLE
            Direct Submission
            Submitted (15-APR-1993) T. Barbeyron, CNRS, Place George Teissier,
  JOURNAL
            29680 Roscoff, FRANCE
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BASE COUNT 787 a 397 c 420 g 576 t ORIGIN

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Db		TCTGGGATGGCTGTAATCAGCAGCAAGTTGCAAATTACCCACTTTATTATACATCGGGTG	
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QУ		CTCGAAATGACTTTCACACCTATGGTGTCAATGTAACTAAAGACAAGATCACTTGGTACG	
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Qу		CATTATCACAAGGCTTACGCGCGCGCATACACAATGGAAATGTAATCAATTTTACCCAT	
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Db			
Qу		CATCAAGCAATAAAAATGTGGCAACTGTGAACAGTGCTGGCGTTGTAAAAAGCTAAAAATA	
Db			
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Qу	1921	TTGCGGTGAATTAAGCTAACTCAAACTAGCCTCGAAGGATTGAGGCACTTTATTTA	1980
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US-09-988-201-6 Title: RESULT 1 I39507 kappa-carraghenase - Alteromonas carrageenovora C; Species: Alteromonas carrageenovora C;Datc: 19-Jul-1996 #sequence revision 19-Jul-1996 #text change 08-Oct-1999 C; Accession: I39507; S40202 R; Barbeyron, T.; Henrissat, B.; Kloareg, B. Gene 139, 105-109, 1994 A; Title: The gene encoding the kappa-carrageenase of Alteromonas carrageenovora is related to beta-1,3-1,4-glucanases. A; Reference number: I39507; MUID: 94156170; PMID: 8112578 A; Accession: I39507 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Residues: 1-397 < RES> A; Cross-references: EMBL: X71620; NID: q437973; PIDN: CAA50624.1; PID: q437974 C: Genetics: A; Gene: cgkA Query Match 64.9%; Score 2116; DB 2; Length 397; Best Local Similarity 100.0%; Pred. No. 7e-136; Matches 397; Conservative 0; Mismatches Indels Gaps 0: Qу 167 MKPISIVAFPIPAISMLLLSAVSQAASMQPPIAKPGETWILQAKRSDEFNVKDATKWNFQ 226 Db 1 MKPISIVAFPIPAISMLLLSAVSQAASMQPPIAKPGETWILQAKRSDEFNVKDATKWNFQ 60 227 TENYGVWSWKNENATVSNGKLKLTTKRESHQRTFWDGCNQQQVANYPLYYTSGVAKSRAT 286 Qу 61 TENYGVWSWKNENATVSNGKLKLTTKRESHQRTFWDGCNQQQVANYPLYYTSGVAKSRAT 120 Db 287 GNYGYYEARIKGASTFPGVSPAFWMYSTIDRSLTKEGDVOYSEIDVVELTOKSAVRESDH 346 Οv 121 GNYGYYEARIKGASTFPGVSPAFWMYSTIDRSLTKEGDVQYSEIDVVELTQKSAVRESDH 180 Db 347 DLHNIVVKNGKPTWMRPGSFPQTNHNGYHLPFDPRNDFHTYGVNVTKDKITWYVDGEIVG 406 Qу 181 DLHNIVVKNGKPTWMRPGSFPQTNHNGYHLPFDPRNDFHTYGVNVTKDKITWYVDGEIVG 240 Db Qу 407 EKDNLYWHRQMNLTLSQGLRAPHTQWKCNQFYPSANKSAEGFPTSMEVDYVRTWVKVGNN 466

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